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EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
S1	1525	west adj nile	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:30
S2	8751	replicon\$	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/21 20:13
S3	126	S1 and S2	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/21 20:16
S4	908	reverse adj genetic\$	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/21 20:16
S5	101781	cDNA	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:30
S6	1526	west adj nile	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:30
S7	723	S6 and S5	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:31
S8	424531	delet\$	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:31
S9	614	S7 and S8	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:31

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S10	300806	envelope\$	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:31
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S12	182065	promoter	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:31
S13	55207	reporter	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:31
S14	324	S11 and S12 and S13	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 20:10
S15	356598	ires	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:32
S16	35	S14 and S15	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:32
S17	910	reverse adj genetics	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 20:10
S18	3829	flavivir\$	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 20:11
S19	74	S17 and S18	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 20:11



results of BLAST

BLASTN 2.2.14 [May-07-2006]
RID: 1148512175-2216-116532263996.BLASTQ1

Database: env_nt
1,047,779 sequences; 1,063,283,128 total letters

Query=
Length=11020

No significant similarity found. For reasons why, [click here](#).

Database: environmental samples
Posted date: May 19, 2006 3:31 AM
Number of letters in database: 1,063,283,128
Number of sequences in database: 1,047,779
Lambda K H
1.33 0.621 1.12
Gapped
Lambda K H
1.33 0.621 1.12
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 1047779
Number of Hits to DB: 17877
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 11020
Length of database: 1063283128
Length adjustment: 32
Effective length of query: 10988
Effective length of database: 1029754200
Effective search space: 11314939149600
Effective search space used: 11314939149600
A: 0
X1: 13 (25.0 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 13 (25.1 bits)
S2: 22 (41.7 bits)



results of BLAST

BLASTN 2.2.14 [May-07-2006]
 RID: 1148511929-7071-210325148673.BLASTQ4

Database: Whole-Genome-Shotgun Sequences
 13,679,503 sequences; 71,237,490,689 total letters

Query=
 Length=11020

No significant similarity found. For reasons why, [click here](#).

Database: Whole-Genome-Shotgun Sequences
 Posted date: May 18, 2006 7:42 PM
 Number of letters in database: -1,837,793,559
 Number of sequences in database: 13,677,712

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 0, Extension: 0
 Number of Sequences: 13677712
 Number of Hits to DB: 1564364
 Number of extensions: 0
 Number of successful extensions: 0
 Number of sequences better than 10: 0
 Number of HSP's better than 10 without gapping: 0
 Number of HSP's gapped: 0
 Number of HSP's successfully gapped: 0
 Length of query: 11020
 Length of database: 71176650469
 Length adjustment: 37
 Effective length of query: 10983
 Effective length of database: 70670575125
 Effective search space: 776174926597875
 Effective search space used: 776174926597875
 A: 0
 X1: 16 (30.8 bits)
 X2: 32 (59.1 bits)
 X3: 54 (99.7 bits)
 S1: 16 (30.7 bits)
 S2: 25 (47.3 bits)



results of BLAST

BLASTN 2.2.14 [May-07-2006]

Query:

Database: nr

Fields: query id, subject ids, % identity, alignment length, mismatches, gap opens, q

100 hits found

1_797	gi 21929238 gb AF404756.1	99.84	11029	9	5	1	11020
1_797	gi 11597239 gb AF196835.2 AF196835	99.78	11029	15	5	1	1
1_797	gi 21929234 gb AF404754.1	99.76	11029	18	5	1	11020
1_797	gi 9930133 gb AF260967.1 AF260967	99.76	11029	18	5	1	1
1_797	gi 77980183 gb AY848696.2	99.75	11029	19	5	1	11020
1_797	gi 50838784 dbj AB185917.1	99.75	11029	19	5	1	11020
1_797	gi 50838782 dbj AB185916.1	99.75	11029	19	5	1	11020
1_797	gi 75859185 gb AY842931.3	99.74	11029	20	5	1	11020
1_797	gi 50872124 dbj AB185914.2	99.74	11029	20	5	1	11020
1_797	gi 77980181 gb AY848695.2	99.73	11029	21	5	1	11020
1_797	gi 77166600 gb DQ211652.1	99.73	11029	21	5	1	11020
1_797	gi 76781535 gb DQ164188.1	99.72	11029	22	5	1	11020
1_797	gi 50872125 dbj AB185915.2	99.72	11029	22	5	1	11020
1_797	gi 66735926 gb DQ066423.1	99.71	11029	23	5	1	11020
1_797	gi 77853218 gb AY848697.2	99.70	11029	24	5	1	11020
1_797	gi 21929236 gb AF404755.1	99.70	11029	24	5	1	11020
1_797	gi 21929232 gb AF404753.1	99.70	11029	24	5	1	11020
1_797	gi 76781547 gb DQ164194.1	99.66	11029	28	5	1	11020
1_797	gi 76781559 gb DQ164200.1	99.65	11029	30	5	1	11020
1_797	gi 26284711 gb AF533540.1	99.65	11029	30	5	1	11020
1_797	gi 76781531 gb DQ164186.1	99.64	11029	31	5	1	11020
1_797	gi 55669121 gb AY646354.1	99.64	11030	30	6	1	11020
1_797	gi 76781549 gb DQ164195.1	99.64	11029	31	5	1	11020
1_797	gi 76781545 gb DQ164193.1	99.64	11029	31	5	1	11020
1_797	gi 59876232 gb AY795965.1	99.62	11029	33	5	1	11020
1_797	gi 76781541 gb DQ164191.1	99.60	11029	35	5	1	11020
1_797	gi 76781571 gb DQ164206.1	99.59	11030	34	7	1	11020
1_797	gi 76781569 gb DQ164205.1	99.59	11029	36	5	1	11020
1_797	gi 76781555 gb DQ164198.1	99.59	11029	36	5	1	11020
1_797	gi 76781553 gb DQ164197.1	99.59	11029	36	5	1	11020
1_797	gi 76781533 gb DQ164187.1	99.58	11029	37	5	1	11020
1_797	gi 55495180 gb AY712948.1	99.57	11029	38	5	1	11020
1_797	gi 71483604 gb DQ080053.1	99.57	11029	38	5	1	11020
1_797	gi 76781551 gb DQ164196.1	99.56	11029	39	5	1	11020
1_797	gi 55495165 gb AY712947.1	99.56	11029	39	5	1	11020
1_797	gi 19387527 gb AF481864.1	99.56	11029	39	5	1	11020
1_797	gi 71483602 gb DQ080052.1	99.56	11029	39	5	1	11020
1_797	gi 76781557 gb DQ164199.1	99.56	11029	39	5	1	11020
1_797	gi 76781537 gb DQ164189.1	99.56	11029	39	5	1	11020
1_797	gi 71483600 gb DQ080051.1	99.56	11029	40	5	1	11020
1_797	gi 7717200 gb AF206518.2 AF206518	99.72	10975	22	5	19	19
1_797	gi 76781543 gb DQ164192.1	99.56	11029	40	5	1	11020
1_797	gi 33948906 gb AY289214.1	99.54	11029	42	5	1	11020
1_797	gi 76781539 gb DQ164190.1	99.54	11029	42	5	1	11020
1_797	gi 71483606 gb DQ080054.1	99.52	11029	44	5	1	11020
1_797	gi 76781563 gb DQ164202.1	99.51	11029	45	5	1	11020
1_797	gi 71483614 gb DQ080058.1	99.51	11029	45	5	1	11020
1_797	gi 71483640 gb DQ080071.1	99.59	11000	36	5	30	11020
1_797	gi 76781567 gb DQ164204.1	99.50	11029	46	5	1	11020
1_797	gi 55495130 gb AY712945.1	99.49	11029	47	5	1	11020
1_797	gi 71483608 gb DQ080055.1	99.52	11018	44	5	1	11009
1_797	gi 71483622 gb DQ080062.1	99.55	11001	40	5	29	11020

1_797	gi 76781565 gb DQ164203.1	99.46	11029	51	5	1	11020
1_797	gi 55495149 gb AY712946.1	99.47	11029	50	5	1	11020
1_797	gi 71483634 gb DQ080068.1	99.54	11001	42	5	29	11020
1_797	gi 71483616 gb DQ080059.1	99.46	11029	51	5	1	11020
1_797	gi 71483630 gb DQ080066.1	99.54	11001	42	5	29	11020
1_797	gi 76781561 gb DQ164201.1	99.45	11029	52	5	1	11020
1_797	gi 71483632 gb DQ080067.1	99.53	11001	43	5	29	11020
1_797	gi 71483610 gb DQ080056.1	99.47	11019	49	5	1	11010
1_797	gi 71483642 gb DQ080072.1	99.53	11000	43	5	30	11020
1_797	gi 71483620 gb DQ080061.1	99.53	11000	43	5	30	11020
1_797	gi 71483636 gb DQ080069.1	99.60	10975	35	5	29	10994
1_797	gi 71483626 gb DQ080064.1	99.52	11001	44	5	29	11020
1_797	gi 71483628 gb DQ080065.1	99.53	10995	43	5	35	11020
1_797	gi 71483638 gb DQ080070.1	99.50	11001	46	5	29	11020
1_797	gi 6581069 gb AF202541.1 AF202541	99.66	10946	26	7	43	
1_797	gi 55975602 gb AY660002.1	99.40	11029	57	5	1	11020
1_797	gi 71483624 gb DQ080063.1	99.53	10975	43	5	29	10994
1_797	gi 71483612 gb DQ080057.1	99.53	10956	43	5	1	10947
1_797	gi 71483618 gb DQ080060.1	99.42	10972	55	5	30	10992
1_797	gi 89148117 gb DQ118127.1	99.12	10969	87	5	1	10960
1_797	gi 33242576 gb AY268133.1	97.97	10990	212	7	21	11000
1_797	gi 30349729 gb AY278441.1	97.27	11001	285	11	1	10989
1_797	gi 89340493 gb DQ411029.1	97.24	10816	280	15	24	10825
1_797	gi 89340495 gb DQ411030.1	97.22	10814	286	11	24	10825
1_797	gi 89340778 gb DQ411031.1	97.21	10814	287	11	24	10825
1_797	gi 87116126 gb DQ377180.1	97.20	10815	286	13	24	10825
1_797	gi 89340786 gb DQ411035.1	97.18	10815	288	13	24	10825
1_797	gi 87083862 gb DQ374652.1	97.23	10793	282	13	24	10803
1_797	gi 89340784 gb DQ411034.1	97.17	10816	287	15	24	10825
1_797	gi 87116124 gb DQ377179.1	97.17	10815	289	13	24	10825
1_797	gi 9930137 gb AF260969.1 AF260969	96.55	11030	369	7	1	
1_797	gi 87116122 gb DQ377178.1	97.16	10816	288	15	24	10825
1_797	gi 87083860 gb DQ374651.1	97.16	10815	290	13	24	10825
1_797	gi 87083864 gb DQ374653.1	97.12	10815	295	13	24	10825
1_797	gi 87083858 gb DQ374650.1	97.12	10815	295	13	24	10825
1_797	gi 89340782 gb DQ411033.1	97.11	10813	299	9	24	10825
1_797	gi 89340780 gb DQ411032.1	97.08	10815	299	13	24	10825
1_797	gi 30230630 gb AY262283.1	96.50	10986	373	8	37	11012
1_797	gi 21929240 gb AF404757.1	96.35	11030	392	7	1	11020
1_797	gi 12744408 gb AF317203.1 AF317203	96.41	10974	381	9	33	
1_797	gi 51011373 gb AY701412.1	96.48	10946	374	7	43	10978
1_797	gi 33242574 gb AY268132.1	96.34	10989	393	5	21	11000
1_797	gi 51011375 gb AY701413.1	96.23	10950	394	15	43	10978
1_797	gi 30349727 gb AY277252.1	96.36	10847	382	9	1	10836
1_797	gi 30349731 gb AY278442.1	96.35	10844	383	9	1	10833
1_797	gi 9930135 gb AF260968.1 AF260968	95.35	11036	490	19	1	
1_797	gi 46277828 gb AY490240.2	95.21	11043	491	34	1	11020
1_797	gi 51318183 gb AY603654.1	94.70	11041	552	29	1	11020



results of BLAST

BLASTN 2.2.14 [May-07-2006]
 RID: 1148511147-28338-105062820528.BLASTQ1

Database: NCBI Transcript Reference Sequences
 652,821 sequences; 1,111,501,987 total letters

Query=
 Length=11020

No significant similarity found. For reasons why, [click here](#).

Database: NCBI Transcript Reference Sequences
 Posted date: May 18, 2006 10:45 PM
 Number of letters in database: 1,111,494,313
 Number of sequences in database: 652,832

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 0, Extension: 0
 Number of Sequences: 652832
 Number of Hits to DB: 522
 Number of extensions: 0
 Number of successful extensions: 0
 Number of sequences better than 10: 0
 Number of HSP's better than 10 without gapping: 0
 Number of HSP's gapped: 0
 Number of HSP's successfully gapped: 0
 Length of query: 11020
 Length of database: 1111494313
 Length adjustment: 32
 Effective length of query: 10988
 Effective length of database: 1090603689
 Effective search space: 11983553334732
 Effective search space used: 11983553334732
 A: 0
 X1: 14 (26.9 bits)
 X2: 32 (59.1 bits)
 X3: 54 (99.7 bits)
 S1: 14 (27.0 bits)
 S2: 22 (41.7 bits)



results of **BLAST**

BLASTN 2.2.14 [May-07-2006]

Query:

Database: refseq_genomic

Fields: query id, subject ids, % identity, alignment length, mismatches, gap opens, q

6 hits found

1_11050	gi 11528013 ref NC_001563.2	79.51	8278	1437	249	1	8153
1_11050	gi 11528013 ref NC_001563.2	90.77	509	37	10	10516	11020
1_11050	gi 9626460 ref NC_001437.1	72.46	3242	622	260	577	3684
1_11050	gi 9626460 ref NC_001437.1	100.00	28	0	0	10789	10816
1_11050	gi 56692441 ref NC_006551.1	76.88	558	60	53	10496	11020
1_11050	gi 9626685 ref NC_001477.1	86.75	83	9	2	9040	9121



results of BLAST

BLASTN 2.2.14 [May-07-2006]

RID: 1148511003-17158-142892004559.BLASTQ4

Database: Genome Survey Sequence, includes single-pass genomic data,
exon-trapped sequences, and Alu PCR sequences.

14,335,827 sequences; 9,038,742,965 total letters

Query=

Length=11020

No significant similarity found. For reasons why, [click here](#).

Database: Genome Survey Sequence, includes single-pass genomic data, exon-trapped
sequences, and Alu PCR sequences.

Posted date: May 18, 2006 8:24 PM

Number of letters in database: 446,610,113

Number of sequences in database: 14,332,659

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 0, Extension: 0

Number of Sequences: 14332659

Number of Hits to DB: 171244

Number of extensions: 0

Number of successful extensions: 0

Number of sequences better than 10: 0

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 0

Number of HSP's successfully gapped: 0

Length of query: 11020

Length of database: 9036544705

Length adjustment: 34

Effective length of query: 10986

Effective length of database: 8549234299

Effective search space: 93921888008814

Effective search space used: 93921888008814

A: 0

X1: 12 (23.1 bits)

X2: 32 (59.1 bits)

X3: 54 (99.7 bits)

S1: 12 (23.3 bits)

S2: 23 (43.6 bits)



results of BLAST

BLASTN 2.2.14 [May-07-2006]
 RID: 1148511297-13266-29868804930.BLASTQ4

Database: Unfinished High Throughput Genomic Sequences; Sequences:
 phases 0,1 and 2
 91,378 sequences; 15,441,179,013 total letters

Query=
 Length=11020

No significant similarity found. For reasons why, [click here](#).

Database: Unfinished High Throughput Genomic Sequences; Sequences: phases 0,1 and 2

Posted date: May 18, 2006 11:01 PM
 Number of letters in database: -1,740,329,326
 Number of sequences in database: 91,362
 Lambda K H
 1.33 0.621 1.12
 Gapped
 Lambda K H
 1.33 0.621 1.12
 Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 0, Extension: 0
 Number of Sequences: 91362
 Number of Hits to DB: 330308
 Number of extensions: 0
 Number of successful extensions: 0
 Number of sequences better than 10: 0
 Number of HSP's better than 10 without gapping: 0
 Number of HSP's gapped: 0
 Number of HSP's successfully gapped: 0
 Length of query: 11020
 Length of database: 15439539854
 Length adjustment: 35
 Effective length of query: 10985
 Effective length of database: 15436342184
 Effective search space: 169568218891240
 Effective search space used: 169568218891240
 A: 0
 X1: 19 (36.5 bits)
 X2: 32 (59.1 bits)
 X3: 54 (99.7 bits)
 S1: 19 (36.2 bits)
 S2: 24 (45.4 bits)



results of BLAST

BLASTN 2.2.14 [May-07-2006]

Query:

Database: pat

Fields: query id, subject ids, % identity, alignment length, mismatches, gap opens, q

44 hits found

1_12764	gi 27647035 emb AX577796.1	99.56	11029	39	5	1	11020
1_12764	gi 27646162 emb AX576542.1	99.56	11029	39	5	1	11020
1_12764	gi 52747867 emb CQ874691.1	99.81	2070	4	0	400	2469
1_12764	gi 52745306 emb CQ871188.1	99.81	2070	4	0	400	2469
1_12764	gi 51997335 emb CQ867049.1	99.81	2070	4	0	400	2469
1_12764	gi 15554477 emb AX224225.1	99.85	2008	3	0	421	2428
1_12764	gi 44845960 emb CQ754934.1	99.73	1483	4	0	918	2400
1_12764	gi 44845959 emb CQ754933.1	99.73	1483	4	0	918	2400
1_12764	gi 44845215 emb CQ753913.1	99.73	1483	4	0	918	2400
1_12764	gi 44845214 emb CQ753912.1	99.73	1483	4	0	918	2400
1_12764	gi 52747866 emb CQ874690.1	99.78	1375	3	0	918	2292
1_12764	gi 44845219 emb CQ753917.1	99.78	1375	3	0	918	2292
1_12764	gi 52747868 emb CQ874692.1	99.91	1101	1	0	2401	3501
1_12764	gi 44845961 emb CQ754935.1	99.91	1101	1	0	2401	3501
1_12764	gi 44845216 emb CQ753914.1	99.91	1101	1	0	2401	3501
1_12764	gi 3964470 gb AR003211.1 AR003211	72.49	3243	619	261	577	
1_12764	gi 3964377 gb AR003118.1 AR003118	72.49	3243	619	261	577	
1_12764	gi 588599 gb I08692.1	72.45	3245	620	262	577	3684
1_12764	gi 2170697 dbj E02466.1	72.16	3261	637	262	558	3684
1_12764	gi 2170908 dbj E02680.1	72.16	3261	637	262	558	3684
1_12764	gi 92829674 dbj DD136821.1	100.00	201	0	0	1028	1228
1_12764	gi 55581982 emb CQ897149.1	96.17	183	0	5	10845	11020
1_12764	gi 55581981 emb CQ897148.1	97.00	100	1	2	10553	10650
1_12764	gi 55581943 emb CQ897110.1	80.33	244	25	21	10708	10946
1_12764	gi 55581947 emb CQ897114.1	79.92	244	26	21	10708	10946
1_12764	gi 55581945 emb CQ897112.1	79.92	244	26	21	10708	10946
1_12764	gi 55581939 emb CQ897106.1	79.92	244	26	21	10708	10946
1_12764	gi 55581950 emb CQ897117.1	79.84	243	26	21	10708	10945
1_12764	gi 55581948 emb CQ897115.1	80.00	235	25	20	10708	10937
1_12764	gi 55581944 emb CQ897111.1	79.59	245	25	22	10708	10946
1_12764	gi 55581949 emb CQ897116.1	80.35	229	22	20	10708	10930
1_12764	gi 55581946 emb CQ897113.1	79.57	235	26	20	10708	10937
1_12764	gi 55581941 emb CQ897108.1	79.27	246	24	25	10708	10946
1_12764	gi 55581942 emb CQ897109.1	82.88	111	10	9	10708	10817
1_12764	gi 55581940 emb CQ897107.1	82.88	111	10	9	10708	10817
1_12764	gi 55581920 emb CQ897087.1	98.08	52	0	1	10905	10955
1_12764	gi 55581919 emb CQ897086.1	98.08	52	0	1	10905	10955
1_12764	gi 27646165 emb AX576545.1	88.24	51	4	2	433	482
1_12764	gi 88500611 dbj DD219684.1	100.00	30	0	0	403	432
1_12764	gi 27646167 emb AX576547.1	100.00	29	0	0	10992	11020
1_12764	gi 15554499 emb AX224249.1	100.00	29	0	0	421	449
1_12764	gi 27646166 emb AX576546.1	100.00	28	0	0	1	28
1_12764	gi 83410046 emb CS196074.1	100.00	28	0	0	10616	10643
1_12764	gi 55581931 emb CQ897098.1	100.00	25	0	0	10791	10815



results of BLAST

BLASTN 2.2.14 [May-07-2006]
 RID: 1148511540-26048-113003772134.BLASTQ4

Database: PDB nucleotide database
 6378 sequences; 414,729 total letters

Query=
 Length=11020

No significant similarity found. For reasons why, [click here](#).

Database: PDB nucleotide database
 Posted date: May 18, 2006 10:45 PM
 Number of letters in database: 412,402
 Number of sequences in database: 6,326

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 0, Extension: 0
 Number of Sequences: 6326
 Number of Hits to DB: 53
 Number of extensions: 0
 Number of successful extensions: 0
 Number of sequences better than 10: 0
 Number of HSP's better than 10 without gapping: 0
 Number of HSP's gapped: 0
 Number of HSP's successfully gapped: 0
 Length of query: 11020
 Length of database: 412402
 Length adjustment: 22
 Effective length of query: 10998
 Effective length of database: 273230
 Effective search space: 3004983540
 Effective search space used: 3004983540
 A: 0
 X1: 9 (17.3 bits)
 X2: 32 (59.1 bits)
 X3: 54 (99.7 bits)
 S1: 9 (17.7 bits)
 S2: 15 (28.8 bits)



results of **BLAST**

BLASTN 2.2.14 [May-07-2006]

Query:

Database: month

Fields: query id, subject ids, % identity, alignment length, mismatches, gap opens, q

6 hits found

1_20047	gi 95140176 emb AJ965631.1	97.32	149	4	0	9122	9270
1_20047	gi 95140170 emb AJ965628.1	97.32	149	4	0	9122	9270
1_20047	gi 95140168 emb AJ965627.1	97.32	149	4	0	9122	9270
1_20047	gi 95140166 emb AJ965626.1	97.32	149	4	0	9122	9270
1_20047	gi 95140174 emb AJ965630.1	96.64	149	5	0	9122	9270
1_20047	gi 95140172 emb AJ965629.1	96.64	149	5	0	9122	9270



results of BLAST

BLASTN 2.2.14 [May-07-2006]
RID: 1148511630-30931-14826378846.BLASTQ1

Database: dbsts
881,195 sequences; 495,721,948 total letters

Query=
Length=11020

No significant similarity found. For reasons why, [click here](#).

Database: Database of GenBank+EMBL+DDBJ sequences from STS Divisions
Posted date: May 19, 2006 5:11 AM
Number of letters in database: 495,721,948
Number of sequences in database: 881,195
Lambda K H
1.33 0.621 1.12
Gapped
Lambda K H
1.33 0.621 1.12
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 881195
Number of Hits to DB: 20596
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 11020
Length of database: 495721948
Length adjustment: 31
Effective length of query: 10989
Effective length of database: 468404903
Effective search space: 5147301479067
Effective search space used: 5147301479067
A: 0
X1: 12 (23.1 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 12 (23.3 bits)
S2: 21 (39.9 bits)



results of BLAST

BLASTN 2.2.14 [May-07-2006]

Query:

Database: chromosome

Fields: query id, subject ids, % identity, alignment length, mismatches, gap opens, q

6 hits found

1_26437	gi 11528013 ref NC_001563.2	79.51	8278	1437	249	1	8153
1_26437	gi 11528013 ref NC_001563.2	90.77	509	37	10	10516	11020
1_26437	gi 9626460 ref NC_001437.1	72.46	3242	622	260	577	3684
1_26437	gi 9626460 ref NC_001437.1	100.00	28	0	0	10789	10816
1_26437	gi 56692441 ref NC_006551.1	76.88	558	60	53	10496	11020
1_26437	gi 9626685 ref NC_001477.1	86.75	83	9	2	9040	9121